

## SEQUENCE LISTING

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JAN 3 0 2004

**TECH CENTER 1600/2900** 

<110> RONSIN, CHRISTOPHE SCOTT, VERONIQUE TRIEBEL, FREDERIC															
<120>	<120> PEPTIDE COMPOUND DERIVED FROM A SHIFTED ORF OF THE ICE GENE														
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Thr Va		Arg	Leu	Phe	Leu	Ala	Trp	Leu	Pro	Cvs	Met	. Met	. Val	Pro	
1			5					10	1	-			15		
Cys Tr	) Leu	Pro 20	Trp	Arg	Thr	Trp	Trp 25	Trp	Ser	Ser	Ser	Ser 30		Ala	
Trp Val	Ser 35	Trp	Ala	Ser	Ser	Ala 40	Leu	Glu	Thr	Ser	Thr 45		Pro	Ala	
Thr Gl <sub>y</sub> 50	Ala	Thr	Trp	Thr	Lys 55	Trp	Leu	His	Tyr	Ala 60	Gly	Ser	Ser	Arg	
Ile Ser 65	Pro	Thr	Leu	Glu 70	Ala	Thr	Leu	Thr	Val 75	Ser	Pro	Phe	Leu	Ala 80	
Ser Leu	Arg	Val	Ala 85	Arg	Val	Сув	Leu	Arg 90	Leu	Leu	Cys	Pro	Pro 95	Tyr	
Pro Lys	Asp	Ser 100	Ser	Thr	Glu	Pro	Ser 105	Trp	Arg	Val	Ala	Trp 110	Pro	Ser	
Cys Pro	Ala 115	Ser	Leu	Pro	Ala	Gln 120	Leu	Met	Ser	Ser	Pro 125	Arg	Trp	Trp	
Pro Thr 130	Cys	Leu	Pro	Val	Thr 135	Lys	Leu	Thr	Leu	Arg 140	Pro	Trp	Trp	Ala	

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Ala Cys Gly Ala Arg Val Lys Arg Arg Phe Leu Gln Leu Thr Ser Leu
 145
                                          155
 Ser Arg
 <210> 2
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 <212> PRT
 <213> Homo sapiens
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 Ser Pro Arg Trp Trp Pro Thr Cys Leu
 <210> 3
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acggtggtgc gcttgttttt ggcatggctt ccttgtatga tggttccatg ctggctgcct 60
tggagaacgt ggtggtggtc atcatccagt accgcctggg tgtcctgggc ttcttcagca 120
ctggagacaa gcacgcaacc ggcaactggg gctacctgga ccaagtggct gcactacgct 180
gggtccagca gaatategee caetttggag geaaccetga eegtgtcaee atttttggeg 240
agtetgeggg tggcaegagt gtgtettege ttgttgtgte ecceatatee caaggactet 300
tecaeggage cateatggag agtggegtgg cecteetgee eggeeteatt geeageteag 360
ctgatgtcat ctccacggtg gtggccaacc tgtctgcctg tgaccaagtt gactctgagg 420
ccctggtggg ctgcctgcgg ggcaagagta aagaggagat tcttgcaatt aacaagcctt 480
tcaagatgat ccccggagtg gtggatgggg tcttcctgcc c
<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer
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                                                                   30
<210> 5
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Met Arg Leu His Arg Leu Arg Ala Arg Leu Ser Ala Val Ala Cys Gly
ett etg etg ett ett gte egg gge eag gge eag gae tea gee agt eee
Leu Leu Leu Leu Val Arg Gly Gln Gly Gln Asp Ser Ala Ser Pro
             20
atc cgg acc aca cac acg ggg cag gtg ctg ggg agt ctt gtc cat gtg
Ile Arg Thr Thr His Thr Gly Gln Val Leu Gly Ser Leu Val His Val
aag ggc gcc aat gcc ggg gtc caa acc ttc ctg gga att cca ttt gcc
Lys Gly Ala Asn Ala Gly Val Gln Thr Phe Leu Gly Ile Pro Phe Ala
aag cca cct cta ggt ccg ctg cga ttt gca ccc cct gag ccc cct gaa
                                                                   240
Lys Pro Pro Leu Gly Pro Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
tct tgg agt gtg agg gat gga acc acc cat ccg gcc atg tgt cta
                                                                   288
Ser Trp Ser Gly Val Arg Asp Gly Thr Thr His Pro Ala Met Cys Leu
cag gac ctc acc gca gtg gag tca gag ttt ctt agc cag ttc aac atg
                                                                   336
Gln Asp Leu Thr Ala Val Glu Ser Glu Phe Leu Ser Gln Phe Asn Met
            100
                                105
acc ttc cct tcc gac tcc atg tct gag gac tgc ctg tac ctc agc atc
                                                                   384
Thr Phe Pro Ser Asp Ser Met Ser Glu Asp Cys Leu Tyr Leu Ser Ile
tac acg ccg gcc cat agc cat gaa ggc tct aac ctg ccg gtg atg gtg
                                                                   432
Tyr Thr Pro Ala His Ser His Glu Gly Ser Asn Leu Pro Val Met Val
                        135
tgg atc cac ggt ggt gcg ctt gtt ttt ggc atg gct tcc ttg tat gat
                                                                  480
Trp Ile His Gly Gly Ala Leu Val Phe Gly Met Ala Ser Leu Tyr Asp
                    150
                                        155
ggt tcc atg ctg gct gcc ttg gag aac gtg gtg gtc atc atc cag
                                                                  528
Gly Ser Met Leu Ala Ala Leu Glu Asn Val Val Val Ile Ile Gln
                                    170
tac cgc ctg ggt gtc ctg ggc ttc ttc agc act gga gac aag cac gca
                                                                  576
Tyr Arg Leu Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Lys His Ala
            180
                                185
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acc Thr	ggc Gly	aac Asn 195	Trp	ggc	tac Tyr	ctg Leu	gac Asp 200	Gln	gtg Val	gct Ala	gca Ala	cta Lev 205	Arg	tgg Trp	gtc Val	624
cag Gln	cag Gln 210	Asn	atc Ile	gcc Ala	cac His	ttt Phe 215	Gly	ggc	aac Asn	cct Pro	gac Asp 220	Arg	gto Val	acc Thr	att Ile	672
ttt Phe 225	Gly	gag Glu	tct Ser	gcg Ala	ggt Gly 230	Gly	acg Thr	agt Ser	gtg Val	ser 235	Ser	ctt Leu	gtt Val	gtg Val	tcc Ser 240	720
ccc Pro	ata Ile	tcc Ser	caa Gln	gga Gly 245	ctc Leu	ttc Phe	cac His	gga Gly	gcc Ala 250	Ile	atg Met	gag Glu	agt Ser	ggc Gly 255		768
gcc Ala	ctc Leu	ctg Leu	ccc Pro 260	ggc Gly	ctc Leu	att Ile	gcc Ala	agc Ser 265	tca Ser	gct Ala	gat Asp	gtc Val	atc Ile 270	Ser	acg Thr	816
gtg Val	gtg Val	gcc Ala 275	aac Asn	ctg Leu	tct Ser	gcc Ala	tgt Cys 280	gac Asp	caa Gln	gtt Val	gac Asp	tct Ser 285	Glu	gcc Ala	ctg Leu	864
gtg Val	ggc Gly 290	tgc Cys	ctg Leu	cgg Arg	ggc Gly	aag Lys 295	agt Ser	aaa Lys	gag Glu	gag Glu	att Ile 300	ctt Leu	gca Ala	att Ile	aac Asn	912
aag Lys 305	cct Pro	ttc Phe	aag Lys	atg Met	atc Ile 310	ccc Pro	gga Gly	gtg Val	gtg Val	gat Asp 315	Gly 999	gtc Val	ttc Phe	ctg Leu	ccc Pro 320	960
agg Arg	cac His	ccc Pro	cag Gln	gag Glu 325	ctg Leu	ctg Leu	gcc Ala	tct Ser	gcc Ala 330	gac Asp	ttt Phe	cag Gln	cct Pro	gtc Val 335	cct Pro	1008
agc Ser	att Ile	gtt Val	ggt Gly 340	gtc Val	aac Asn	aac Asn	aat Asn	gaa Glu 345	ttc Phe	ggc Gly	tgg Trp	ctc Leu	atc Ile 350	ccc Pro	aag Lys	1056
gtc Val	atg Met	agg Arg 355	atc Ile	tat Tyr	gat Asp	acc Thr	cag Gln 360	aag Lys	gaa Glu	atg Met	gac Asp	aga Arg 365	gag Glu	gcc Ala	tcc Ser	1104
cag Gln	gct Ala 370	gct Ala	ctg Leu	cag Gln	Lys	atg Met 375	tta Leu	acg Thr	ctg Leu	ctg Leu	atg Met 380	ttg Leu	cct Pro	cct Pro	aca Thr	1152
ttt Phe 385	ggt Gly	gac Asp	ctg Leu	Leu	agg Arg 390	gag Glu	gag Glu	tac Tyr	Ile	999 Gly 395	gac Asp	aat Asn	999 999	gat Asp	ccc Pro 400	1200
cag Gln	acc Thr	ctc Leu	Gln	gcg Ala 405	cag Gln	ttc Phe	cag Gln	Glu	atg Met 410	atg Met	gcg Ala	gac Asp	tcc Ser	atg Met 415	ttt Phe	1248

gtg Val	atc Ile	cct Pro	gca Ala 420	Leu	caa Gln	gta Val	gca Ala	cat His 425	Phe	caç Glr	g tgt n Cys	tcc Ser	cgc Arg 430	Ala	cct Pro	1296
gtg Val	tac Tyr	ttc Phe 435	Tyr	gag Glu	ttc Phe	cag Gln	cat His 440	Gln	Pro	ago Ser	tgg Trp	ctc Leu 445	Lys	aac Asr	atc lle	1344
agg Arg	cca Pro 450	ccg Pro	cac His	atg Met	aag Lys	gca Ala 455	Asp	cat His	ggt Gly	gat Asp	gag Glu 460	Leu	cct Pro	ttt Phe	gtt Val	1392
ttc Phe 465	aga Arg	agt Ser	ttc Phe	ttt Phe	999 Gly 470	ggc Gly	aac Asn	tac Tyr	att	aaa Lys 475	Phe	act Thr	gag Glu	gaa Glu	gag Glu 480	1440
gag Glu	cag Gln	cta Leu	agc Ser	agg Arg 485	aag Lys	atg Met	atg Met	aag Lys	tac Tyr 490	Trp	gcc Ala	aac Asn	ttt Phe	gcg Ala 495	aga Arg	1488
aat Asn	gly ggg	aac Asn	ccc Pro 500	aat Asn	ggc Gly	gag Glu	ggt Gly	ctg Leu 505	cca Pro	cac His	tgg Trp	ccg Pro	ctg Leu 510	ttc Phe	gac Asp	1536
cag Gln	gag Glu	gag Glu 515	caa Gln	tac Tyr	ctg Leu	cag Gln	ctg Leu 520	aac Asn	cta Leu	cag Gln	cct Pro	gcg Ala 525	gtg Val	ggc Gly	cgg Arg	1584
gct Ala	ctg Leu 530	aag Lys	gcc Ala	cac His	agg Arg	ctc Leu 535	cag Gln	ttc Phe	tgg Trp	aag Lys	aag Lys 540	gcg Ala	ctg Leu	ccc Pro	caa Gln	1632
aag Lys 545	atc Ile	cag Gln	gag Glu	ctc Leu	gag Glu 550	gag Glu	cct Pro	gaa Glu	gag Glu	aga Arg 555	cac His	aca Thr	gag Glu	ctg Leu	tag	1680
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Leu	Leu	Leu	Leu 20	Leu	Val .	Arg	Gly	Gln 25	Gly	Gln	Asp	Ser	Ala 30	Ser	Pro	
Ile	Arg '	Thr 35	Thr	His	Thr	Gly	Gln 40	Val	Leu	Gly	Ser	Leu 45	Val	His	Val	
Lys (	Gly 2 50	Ala .	Asn .	Ala	Gly '	Val 55	Gln	Thr	Phe	Leu	Gly 60	Ile	Pro	Phe	Ala	

Lys Pro Pro Leu Gly Pro Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu 65 70 75 80

- Ser Trp Ser Gly Val Arg Asp Gly Thr Thr His Pro Ala Met Cys Leu 85 90 95
- Gln Asp Leu Thr Ala Val Glu Ser Glu Phe Leu Ser Gln Phe Asn Met 100 105 110
- Thr Phe Pro Ser Asp Ser Met Ser Glu Asp Cys Leu Tyr Leu Ser Ile 115 120 125
- Tyr Thr Pro Ala His Ser His Glu Gly Ser Asn Leu Pro Val Met Val 130 135 140
- Trp Ile His Gly Gly Ala Leu Val Phe Gly Met Ala Ser Leu Tyr Asp 145 150 155 160
- Gly Ser Met Leu Ala Ala Leu Glu Asn Val Val Val Ile Ile Gln 165 170 175
- Tyr Arg Leu Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Lys His Ala 180 185 190
- Thr Gly Asn Trp Gly Tyr Leu Asp Gln Val Ala Ala Leu Arg Trp Val 195 200 205
- Gln Gln Asn Ile Ala His Phe Gly Gly Asn Pro Asp Arg Val Thr Ile 210 215 220
- Phe Gly Glu Ser Ala Gly Gly Thr Ser Val Ser Ser Leu Val Val Ser 225 230 235 240
- Pro Ile Ser Gln Gly Leu Phe His Gly Ala Ile Met Glu Ser Gly Val 245 250 255
- Ala Leu Leu Pro Gly Leu Ile Ala Ser Ser Ala Asp Val Ile Ser Thr 260 265 270
- Val Val Ala Asn Leu Ser Ala Cys Asp Gln Val Asp Ser Glu Ala Leu 275 280 285
- Val Gly Cys Leu Arg Gly Lys Ser Lys Glu Glu Ile Leu Ala Ile Asn 290 295 300
- Lys Pro Phe Lys Met Ile Pro Gly Val Val Asp Gly Val Phe Leu Pro 305 310 315 320
- Arg His Pro Gln Glu Leu Leu Ala Ser Ala Asp Phe Gln Pro Val Pro 325 330 335
- Ser Ile Val Gly Val Asn Asn Glu Phe Gly Trp Leu Ile Pro Lys 340 345 350
- Val Met Arg Ile Tyr Asp Thr Gln Lys Glu Met Asp Arg Glu Ala Ser 355 360 365
- Gln Ala Ala Leu Gln Lys Met Leu Thr Leu Leu Met Leu Pro Pro Thr 370 375 380

Phe Gly Asp Leu Leu Arg Glu Glu Tyr Ile Gly Asp Asn Gly Asp Pro 385 390 395 400

Gln Thr Leu Gln Ala Gln Phe Gln Glu Met Met Ala Asp Ser Met Phe 405 410 415

Val Ile Pro Ala Leu Gln Val Ala His Phe Gln Cys Ser Arg Ala Pro 420 425 430

Val Tyr Phe Tyr Glu Phe Gln His Gln Pro Ser Trp Leu Lys Asn Ile 435 440 445

Arg Pro Pro His Met Lys Ala Asp His Gly Asp Glu Leu Pro Phe Val 450 455

Phe Arg Ser Phe Phe Gly Gly Asn Tyr Ile Lys Phe Thr Glu Glu Glu 465 470 475 480

Glu Gln Leu Ser Arg Lys Met Met Lys Tyr Trp Ala Asn Phe Ala Arg 485 490 495

Asn Gly Asn Pro Asn Gly Glu Gly Leu Pro His Trp Pro Leu Phe Asp 500 505 510

Gln Glu Glu Gln Tyr Leu Gln Leu Asn Leu Gln Pro Ala Val Gly Arg 515 520 525

Ala Leu Lys Ala His Arg Leu Gln Phe Trp Lys Lys Ala Leu Pro Gln 530 535 540

Lys Ile Gln Glu Leu Glu Glu Pro Glu Glu Arg His Thr Glu Leu 545 550 555

<210> 8

<211> 166

<212> PRT

<213> Homo sapiens

<400> 8

Trp Cys Gly Ser Thr Val Val Arg Leu Phe Leu Ala Trp Leu Pro Cys
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Met Met Val Pro Cys Trp Leu Pro Trp Arg Thr Trp Trp Trp Ser Ser 20 25 30

Ser Ser Thr Ala Trp Val Ser Trp Ala Ser Ser Ala Leu Glu Thr Ser 35 40 45

Thr Gln Pro Ala Thr Gly Ala Thr Trp Thr Lys Trp Leu His Tyr Ala
50 55 60

Gly Ser Ser Arg Ile Ser Pro Thr Leu Glu Ala Thr Leu Thr Val Ser
65 70 75 80

Pro Phe Leu Ala Ser Leu Arg Val Ala Arg Val Cys Leu Arg Leu Leu 85 90 95 Cys Pro Pro Tyr Pro Lys Asp Ser Ser Thr Glu Pro Ser Trp Arg Val

Ala Trp Pro Ser Cys Pro Ala Ser Leu Pro Ala Gln Leu Met Ser Ser 115 120 . 125

Pro Arg Trp Trp Pro Thr Cys Leu Pro Val Thr Lys Leu Thr Leu Arg

Pro Trp Trp Ala Ala Cys Gly Ala Arg Val Lys Arg Arg Phe Leu Gln 145 150 155 160

Leu Thr Ser Leu Ser Arg 165

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

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